SEQUENCE LISTING

(1) GENERAL INFORMATION:

   (i) APPLICANT: Role, Lorna W.

   (ii) TITLE OF INVENTION: SPLICE VARIANTS OF THE HEREGULIN GENE, nARIA,

                        AND USES THEREOF

   (iii) NUMBER OF SEQUENCES: 4

   (iv) CORRESPONDENCE ADDRESS:
       (A) ADDRESSEE: Cooper & Dunham LLP
       (B) STREET: 1185 Avenue of the Americas
       (C) CITY: New York
       (D) STATE: New York
       (E) COUNTRY: U.S.A.
       (F) ZIP: 10036

   (v) COMPUTER READABLE FORM:
       (A) MEDIUM TYPE: Floppy disk
       (B) COMPUTER: IBM PC compatible
       (C) OPERATING SYSTEM: PC-DOS/MS-DOS
       (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

   (vi) CURRENT APPLICATION DATA:
       (A) APPLICATION NUMBER:
       (B) FILING DATE:
       (C) CLASSIFICATION:

   (viii) ATTORNEY/AGENT INFORMATION:
       (A) NAME: White, John P.
       (B) REGISTRATION NUMBER: 28,678
       (C) REFERENCE/DOCKET NUMBER: 46839-A

   (ix) TELECOMMUNICATION INFORMATION:
       (A) TELEPHONE: 212-278-0400
       (B) TELEFAX: 212-391-0526

(2) INFORMATION FOR SEQ ID NO:1:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 3212 base pairs
       (B) TYPE: nucleic acid
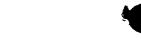   (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGATGCTGC TGCTACTGTC ACTTCTGCCG CTGCCGCTGT TGTTACAGAT TTTGCTTTTG
60

CTCCTTCTAC CGCATGACAA TTGTTTTCCT CGCCTAAGCA GATACCAGCC TCAGATGCTC
120

AAGGTGAGAG TCTTGCCTTT CGCTCTGGGC TATTGGTTCA CTTAATCCGG TCAATTTGTT
180

CGCTGCTCGT GGTTGTCTTT CTCCCCGCCC TCCTTCCCCC TGTTTTGTTT TGTTTCGCTT
240

GCTTTCGGGG GGACGCTCCT TCCCTCAGTC AGAAGAGCTG GAATTGCTTG AGAGGCGTAT
300

AAGGAATTAT AAAAGTGGCC AGGAAACACG AGCGCAGTGA CTGCAGAGCT GCCCTTGGCT
360

TCGGCAAGGC AGCGTGAGCG GCAGAGGGCT CGGGCAGGGG GCGGGGGGTC TCCTTTTTCC
420

CGTGCGTTCC TCTTCTCCCA GTTCGGATGA TGTTGCTGTT TCGGACCTCT CGCTGACTCC
480

TGCCCTGTGA TTTTTGCTGA GCGCTGTGAC TGTTACTCCG TCTCTTTCTG TCTGTGTTTC
540

ACAGTAATGG ACTGTGATAG AGTTAAGGCC TTTTGGAGGT GAGCTGTGTC ACAGCTGATG
600

CTTAAACATG TCTGAAGTAG GCACCGAGAC TTTCCCCAGC CCCTCGGCTC AGCTGAGCCC
660

TGATGCATCC CTTGGCGGGC TCCCGGCTGA GGAGAACATG CCGGGGCCCC ACAGAGAGGA
720

CAGCAGGGTC CCAGGTGTGG CAGGCCTGGC CTCGACCTGC TGCGTGTGCC TGGAAGCAGA
780

GCGACTGAAG GGCTGCCTCA ACTCTGAGAA GATCTGCATC GCCCCTATCC TGGCTTGCCT
840

GCTCAGCCTC TGCCTCTGCA TTGCTGGCCT CAAGTGGGTC TTTGTGGACA AGATTTTTGA
900

GTATGACTCT CCTACACACC TTGACCCTGG GAGGATAGGA CAAGACCCAA GGAGCACTGT
960

GGATCCTACA GCTCTGTCTG CCTGGGTGCC TTCGGAGGTG TATGCCTCAC CCTTCCCCAT

1020

ACCTAGCCTT GAGAGCAAGG CTGAAGTGAC AGTGCAAACT GACAGCTCGC TCGTGCCCTC
1080

CAGGCCCTTC CTTCAGCCTT CTCTCTACAA CCGCATCCTA GATGTCGGGT TGTGGTCCTC
1140

TGCCACACCG TCACTGTCAC CATCCTCCCT GGAGCCTACC ACGGCATCTC AGGCACAAGC
1200

AACAGAAACC AATCTCCAAA CTGCTCCAAA ACTTTCCACT TCTACATCTA CAACTGGGAC
1260

AAGTCATCTC ACAAAATGTG ACATAAAGCA GAAAGCCTTC TGTGTAAATG GGGGAGAGTG
1320

CTACATGGTT AAAGACCTCC CAAACCCTCC ACGATACCTA TGCAGGTGCC CAAATGAATT
1380

TACTGGTGAT CGCTGCCAAA ACTACGTAAT GGCCAGCTTC TACAAGCATC TTGGGATTGA
1440

ATTTATGGAA GCTGAGGAAC TGTACCAGAA ACGGGTGCTG ACCATAACTG GCATTTGCAT
1500

TGCTCTTCTA GTAGTTGGCA TCATGTGTGT GGTGGCCTAC TGCAAAACCA AGAAGCAGAG
1560

GAAAAAGTTG CATGACCGCC TTCGGCAGAG CCTTCGCTCA GAGAGGAACA ACGTTATGAA
1620

CATGGCAAAT GGGCCACACC ACCCCAACCC ACCACCAGAC AATGTCCAGC TGGTGAATCA
1680

GTACGTTTCA AAAAACATAA TCTCCAGTGA ACGTGTCGTT GAGCGAGAAA CCGAGACCTC
1740

GTTTTCCACA AGCCACTACA CCTCAACAAC TCATCACTCC ATGACAGTCA CCCAGACGCC
1800

TAGCCACAGC TGGAGTAATG GCCATACCGA AAGCATTCTC TCCGAAAGCC ACTCCGTGCT
1860

CGTCAGCTCC TCAGTGGAGA ATAGCAGGCA CACCAGCCCA ACAGGGCCAC GAGGCCGCCT
1920

CAATGGCATT GGTGGGCCAA GGGAAGGCAA CAGCTTCCTC CGGCATGCAA GAGAGACCCC
1980

TGACTCCTAC CGAGACTCTC CTCACAGTGA AAGGTATGTC TCAGCTATGA CCACACCAGC
2040

TCGCATGTCA CCCGTTGATT TCCACACTCC AACTTCTCCC AAGTCCCCTC CATCTGAAAT
2100

GTCACCACCA GTTTCCAGCT TGACCATCTC CATCCCTTCG GTGGCGGTGA GTCCCTTTAT
2160

GGACGAGGAG AGACCGCTGC TGTTGGTGAC CCCACCACGG CTGCGTGAGA AGTACGACAA
2220

CCACCTTCAG CAATTCAACT CCTTCCACAA CAATCCCACC CATGAGAGCA ACAGTCTGCC
2280

ACCCAGTCCT CTGAGGATAG TGGAGGATGA AGAGTATGAG ACCACGCAGG AGTACGAACC
2340

AGCACAGGAG CCTCCAAAGA AACTCACCAA CAGCCGGAGG GTGAAAGAA CAAAGCCCAA
2400

TGGCCATATT TCCAGCAGGG TAGAAGTGGA CTCCGACACA AGCTCTCAGA GCACTAGCTC
2460

TGAGAGCGAA ACAGAAGATG AAAGAATAGG TGAGGATACA CCATTTCTTA GCATACAAAA
2520

TCCCATGGCA ACCAGTCTGG AGCCAGCCGC TGCATATCGG CTGGCTGAGA ACAGGACTAA
2580

CCCGGCAAAT CGCTTCTCCA CACCAGAAGA GTTGCAAGCA AGGTTGTCCA GTGTAATAGC
2640

TAACCAAGAC CCTATTGCTG TATAAGACAT AAACAAAACA CATAGATTCA CATGTAAAAC
2700

TTTATTTTAT ATAATGAAGT ATTCCACCTT TAAATTAAAC AATTTATTTT ATTTTAGCAA
2760

TTCCGCTGAT AGAAAACAAG AGTGGAAAAA GAAACTTTTA TAAATTAAGT ATACGTATGT
2820

ACAAATGTGT TATGTGCCAT ATGTAGCAAT TTTTTACAGT ATTTCCAAAA TGGGGAAAGA
2880

TATCAATGGT GCCTTTATGT TATGTTATGT TGAGAGCAAG TTTTGTACAG CTACAATGAT
2940

TGCTGTCCCG TAGTATTTTG CAAAACCTTC TAGCCCTCAG TTGTTCTGGC TTTTTTGTGC
3000

ATTGCATTAT AATGACTGGA TGTATGATTT GCAAGAATTG CAGAAGTCCC CATTTGCTTG
3060

TTGTGGAATC CCCAGATCAA AAAGCCCTGT TATGGCACTC ACACCCTATC CACTTCACCA

3120

GGAAAAAAAA AAAATCAAAA AAAAAAAAAA AAAAAAAAGA AAAGAAAGAG AAAAAAGAAA
3180

AGAAAAAGAA AAAAAAAGCT GAAAAAATAA AA
3212

(2) INFORMATION FOR SEQ ID NO:2:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1070 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Arg
      Gly Cys Cys Cys Tyr Cys His Phe Cys Arg Cys Arg Cys Cys Tyr
      1   5   10   15

Xaa
      Phe Cys Phe Cys Ser Phe Tyr Arg Met Thr Ile Val Phe Leu Ala
            20   25   30

Leu
      Ala Asp Thr Ser Leu Arg Cys Ser Arg Xaa Glu Ser Cys Leu Ser
         35   40   45

Gly
      Trp Ala Ile Gly Ser Leu Asn Pro Val Asn Leu Phe Ala Ala Arg
        50   55   60

Leu
      Cys Leu Ser Pro Arg Pro Pro Ser Pro Cys Phe Val Leu Phe Arg
      65   70   75   80

Leu
      Leu Ser Gly Gly Arg Ser Phe Pro Gln Ser Glu Glu Leu Glu Leu
            85   90   95

Gln   Glu Arg Arg Ile Arg Asn Tyr Lys Ser Gly Gln Glu Thr Arg Ala
                   100   105   110

Arg   Xaa Leu Gln Ser Cys Pro Trp Leu Arg Gln Gly Ser Val Ser Gly
                   115   120   125

Ser   Gly Leu Gly Gln Gly Ala Gly Gly Leu Leu Phe Pro Val Arg Ser
                   130   135   140

Pro   Ser Pro Ser Ser Asp Asp Val Ala Val Ser Asp Leu Ser Leu Thr
160   145   150   155

Ser   Ala Leu Xaa Phe Leu Leu Ser Ala Val Thr Val Thr Pro Ser Leu
                       165   170   175

Gly   Val Cys Val Ser Gln Xaa Trp Thr Val Ile Glu Leu Arg Pro Phe
                       180   185   190

Thr   Gly Glu Leu Cys His Ser Xaa Cys Leu Asn Met Ser Glu Val Gly
                   195   200   205

Leu   Glu Thr Phe Pro Ser Pro Ser Ala Gln Leu Ser Pro Asp Ala Ser
                   210   215   220

Asp   Gly Gly Leu Pro Ala Glu Glu Asn Met Pro Gly Pro His Arg Glu
240   225   230   235

Cys   Ser Arg Val Pro Gly Val Ala Gly Leu Ala Ser Thr Cys Cys Val
                       245   250   255

Cys   Leu Glu Ala Glu Arg Leu Lys Gly Cys Leu Asn Ser Glu Lys Ile

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                    260                       265                        270
         Ile Ala Pro Ile Leu Ala Cys Leu Leu Ser Leu Cys Leu Cys Ile
Ala
             275                   280                     285
         Gly Leu Lys Trp Val Phe Val Asp Lys Ile Phe Glu Tyr Asp Ser
Pro
             290                   295                     300
         Thr His Leu Asp Pro Gly Arg Ile Gly Gln Asp Pro Arg Ser Thr
Val
320      305                   310                     315
         Asp Pro Thr Ala Leu Ser Ala Trp Val Pro Ser Glu Val Tyr Ala
Ser
                     325                   330                     335
         Pro Phe Pro Ile Pro Ser Leu Glu Ser Lys Ala Glu Val Thr Val
Gln
                 340                   345                     350
         Thr Asp Ser Ser Leu Val Pro Ser Arg Pro Phe Leu Gln Pro Ser
Leu
                 355                   360                     365
         Tyr Asn Arg Ile Leu Asp Val Gly Leu Trp Ser Ser Ala Thr Pro
Ser
             370                   375                     380
         Leu Ser Pro Ser Ser Leu Glu Pro Thr Thr Ala Ser Gln Ala Gln
Ala
400      385                   390                     395
         Thr Glu Thr Asn Leu Gln Thr Ala Pro Lys Leu Ser Thr Ser Thr
Ser
                 405                   410                     415
         Thr Thr Gly Thr Ser His Leu Thr Lys Cys Asp Ile Lys Gln Lys
Ala
                 420                   425                     430
```

Asn   Phe Cys Val Asn Gly Gly Glu Cys Tyr Met Val Lys Asp Leu Pro
                435   440   445

Arg   Pro Pro Arg Tyr Leu Cys Arg Cys Pro Asn Glu Phe Thr Gly Asp
                450   455   460

Glu   Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Lys His Leu Gly Ile
480   465   470   475

Thr   Phe Met Glu Ala Glu Glu Leu Tyr Gln Lys Arg Val Leu Thr Ile
                      485   490   495

Ala   Gly Ile Cys Ile Ala Leu Leu Val Val Gly Ile Met Cys Val Val
                    500   505   510

Arg   Tyr Cys Lys Thr Lys Lys Gln Arg Lys Lys Leu His Asp Arg Leu
                515   520   525

Gly   Gln Ser Leu Arg Ser Glu Arg Asn Asn Val Met Asn Met Ala Asn
                530   535   540

Gln   Pro His His Pro Asn Pro Pro Pro Asp Asn Val Gln Leu Val Asn
560   545   550   555

Glu   Tyr Val Ser Lys Asn Ile Ile Ser Ser Glu Arg Val Val Glu Arg
                      565   570   575

His   Thr Glu Thr Ser Phe Ser Thr Ser His Tyr Thr Ser Thr Thr His
                      580   585   590

His   Ser Met Thr Val Thr Gln Thr Pro Ser His Ser Trp Ser Asn Gly

```
                 595                         600                         605

     Thr Glu Ser Ile Leu Ser Glu Ser His Ser Val Leu Val Ser Ser
Ser
                 610                         615                 620

     Val Glu Asn Ser Arg His Thr Ser Pro Thr Gly Pro Arg Gly Arg
Leu
                 625                     630                 635
640
     Asn Gly Ile Gly Gly Pro Arg Glu Gly Asn Ser Phe Leu Arg His
Ala
                             645                     650                 655

     Arg Glu Thr Pro Asp Ser Tyr Arg Asp Ser Pro His Ser Glu Arg
Tyr
                         660                     665                 670

     Val Ser Ala Met Thr Thr Pro Ala Arg Met Ser Pro Val Asp Phe
His
                     675                     680                 685

     Thr Pro Thr Ser Pro Lys Ser Pro Pro Ser Glu Met Ser Pro Pro
Val
                 690                     695                 700

     Ser Ser Leu Thr Ile Ser Ile Pro Ser Val Ala Val Ser Pro Phe
Met
                 705                     710                 715
720
     Asp Glu Glu Arg Pro Leu Leu Leu Val Thr Pro Pro Arg Leu Arg
Glu
                         725                     730                 735

     Lys Tyr Asp Asn His Leu Gln Gln Phe Asn Ser Phe His Asn Asn
Pro
                         740                     745                 750

     Thr His Glu Ser Asn Ser Leu Pro Pro Ser Pro Leu Arg Ile Val
Glu
                     755                     760                 765
```

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Pro     Asp Glu Glu Tyr Glu Thr Thr Gln Glu Tyr Glu Pro Ala Gln Glu
             770             775             780

Asn     Pro Lys Lys Leu Thr Asn Ser Arg Arg Val Lys Arg Thr Lys Pro
800          785             790             795

Gln     Gly His Ile Ser Ser Arg Val Glu Val Asp Ser Asp Thr Ser Ser
                     805             810             815

Asp     Ser Thr Ser Ser Glu Ser Glu Thr Glu Asp Glu Arg Ile Gly Glu
                     820             825             830

Pro     Thr Pro Phe Leu Ser Ile Gln Asn Pro Met Ala Thr Ser Leu Glu
                     835             840             845

Arg     Ala Ala Ala Tyr Arg Leu Ala Glu Asn Arg Thr Asn Pro Ala Asn
                     850             855             860

Ala     Phe Ser Thr Pro Glu Glu Leu Gln Ala Arg Leu Ser Ser Val Ile
880          865             870             875

Phe     Asn Gln Asp Pro Ile Ala Val Xaa Asp Ile Asn Lys Thr His Arg
                     885             890             895

Leu     Thr Cys Lys Thr Leu Phe Tyr Ile Met Lys Tyr Ser Thr Phe Lys
                     900             905             910

Trp     Asn Asn Leu Phe Tyr Phe Ser Asn Ser Ala Asp Arg Lys Gln Glu
                     915             920             925

Tyr     Lys Lys Lys Leu Leu Xaa Ile Lys Tyr Thr Tyr Val Gln Met Cys
```

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                      930                          935                              940

         Val Pro Tyr Val Ala Ile Phe Tyr Ser Ile Ser Lys Met Gly Lys
Asp
         945                          950                          955
960
         Ile Asn Gly Ala Phe Met Leu Cys Tyr Val Glu Ser Lys Phe Cys
Thr
                          965                          970                          975

         Ala Thr Met Ile Ala Val Pro Xaa Tyr Phe Ala Lys Pro Ser Ser
Pro
                          980                          985                          990

         Gln Leu Phe Trp Leu Phe Cys Ala Leu His Tyr Asn Asp Trp Met
Tyr
                          995                          1000                         1005

         Asp Leu Gln Glu Leu Gln Lys Ser Pro Phe Ala Cys Cys Gly Ile
Pro
             1010                         1015                         1020

         Arg Ser Lys Ser Pro Val Met Ala Leu Thr Pro Tyr Pro Leu His
Gln
         1025                         1030                         1035
1040
         Glu Lys Lys Lys Ile Lys Lys Lys Lys Lys Lys Arg Lys Glu
Arg
                          1045                         1050                         1055

         Glu Lys Arg Lys Glu Lys Glu Lys Lys Ser Xaa Lys Asn Lys
                  1060                         1065                         1070
```

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1351 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGGCCTGTAA GATGCTGTAT CATTTGGTTG GGGGGGCCTC TGCGTGGTAA TGGACCGTGA
60

GAGCGGCCAG GCCTTCTTCT GGAGGTGAGC CGATGGAGAT TTATTCCCCA GACATGTCTG
120

AGGTCGCCGC CGAGAGGTCC TCCAGCCCCT CCACTCAGCT GAGTGCAGAC CCATCTCTTG
180

ATGGGCTTCC GGCAGCAGAA GACATGCCAG AGCCCCAGAC TGAAGATGGG AGAACCCCTG
240

GACTCGTGGG CCTGGCCGTG CCCTGCTGTG CGTGCCTAGA AGCTGAGCGC CTGAGAGGTT
300

GCCTCAACTC AGAGAAAATC TGCATTGTCC CCATCCTGGC TTGCCTGGTC AGCCTCTGCC
360

TCTGCATCGC CGGCCTCAAG TGGGTATTTG TGGACAAGAT CTTTGAATAT GACTCTCCTA
420

CTCACCTTGA CCCTGGGGGG TTAGGCCAGG ACCCTATTAT TTCTCTGGAC GCAACTGCTG
480

CCTCAGCTGT GTGGGTGTCG TCTGAGGCAT ACACTTCACC TGTCTCTAGG GCTCAATCTG
540

AAAGTGAGGT TCAAGTTACA GTGCAAGGTG ACAAGGCTGT TGTCTCCTTT GAACCATCAG
600

CGGCACCGAC ACCGAAGAAT CGTATTTTTG CCTTTTCTTT CTTGCCGTCC ACTGCGCCAT
660

CCTTCCCTTC ACCCACCCGG AACCCTGAGG TGAGAACGCC CAAGTCAGCA ACTCAGCCAC
720

AAACAACAGA AACTAATCTC CAAACTGCTC CTAAACTTTC TACATCTACA TCCACCACTG
780

GGACAAGCCA TCTTGTAAAA TGTGCGGAGA AGGAGAAAAC TTTCTGTGTG AATGGAGGGG
840

AGTGCTTCAT GGTGAAAGAC CTTTCAAACC CCTCGAGATA CTTGTGCAAA GGCGGAGGAG
900

CTGTACCAGA AGAGAGTGCT GACCATAACC GGCATCTGCA TCGCCCTCCT TGTGGTCGGC
960

ATCATGTGTG TGGTGGCCTA CTGCAAAACC AAGAACAGC GGAAAAAGCT GCATGACCGT
1020

CTTCGGCAGA GCCTTCGGTC TGAACGAAAC AATACGATGA ACATTGCCAA TGGGCCTCAC
1080

CATCCTAACC CACCCCCCGA GAATGTCCAG CTGGTGAATC AATACGTATC TAAAAACGTC
1140

ATCTCCAGTG AGCATATTGT TGAGAGAGAA GCAGAGACAT CCTTTTCCAC CAGTCACTAT
1200

ACTTCCACAG CCCATCACTC CACTACTGTC ACCCAGACTC CTAGCCACAG CTGGAGCAAC
1260

GGACACACTG AAAGCATCCT TTCCGAAAGC CACTCTGTAA TCGTGATGTC ATCCGTAGAA
1320

AACAGTAGGC ACAGCAGCCC AACTGGGGCC G
1351

(2) INFORMATION FOR SEQ ID NO:4:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 449 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
      Ala Cys Lys Met Leu Tyr His Leu Val Gly Gly Ala Ser Ala Trp
Xaa
      1               5                   10                  15


      Trp Thr Val Arg Ala Ala Arg Pro Ser Ser Gly Gly Glu Pro Met
Glu
                  20                  25                  30


      Ile Tyr Ser Pro Asp Met Ser Glu Val Ala Ala Glu Arg Ser Ser
Ser
                  35                  40                  45


      Pro Ser Thr Gln Leu Ser Ala Asp Pro Ser Leu Asp Gly Leu Pro
Ala
                  50                  55                  60
```

Gly   Ala Glu Asp Met Pro Glu Pro Gln Thr Glu Asp Gly Arg Thr Pro
65   70   75   80

Arg   Leu Val Gly Leu Ala Val Pro Cys Cys Ala Cys Leu Glu Ala Glu
85   90   95

Leu   Leu Arg Gly Cys Leu Asn Ser Glu Lys Ile Cys Ile Val Pro Ile
100   105   110

Val   Ala Cys Leu Val Ser Leu Cys Leu Cys Ile Ala Gly Leu Lys Trp
115   120   125

Pro   Phe Val Asp Lys Ile Phe Glu Tyr Asp Ser Pro Thr His Leu Asp
130   135   140

Ala   Gly Gly Leu Gly Gln Asp Pro Ile Ile Ser Leu Asp Ala Thr Ala
160   145   150   155

Arg   Ser Ala Val Trp Val Ser Ser Glu Ala Tyr Thr Ser Pro Val Ser
165   170   175

Ala   Ala Gln Ser Glu Ser Glu Val Gln Val Thr Val Gln Gly Asp Lys
180   185   190

Ile   Val Val Ser Phe Glu Pro Ser Ala Ala Pro Thr Pro Lys Asn Arg
195   200   205

Pro   Phe Ala Phe Ser Phe Leu Pro Ser Thr Ala Pro Ser Phe Pro Ser
210   215   220

Gln   Thr Arg Asn Pro Glu Val Arg Thr Pro Lys Ser Ala Thr Gln Pro

225 230 235
240

Thr   Thr Thr Glu Thr Asn Leu Gln Thr Ala Pro Lys Leu Ser Thr Ser

                     245 250 255

Lys   Ser Thr Thr Gly Thr Ser His Leu Val Lys Cys Ala Glu Lys Glu

             260 265 270

Ser   Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met Val Lys Asp Leu

             275 280 285

Glu   Asn Pro Ser Arg Tyr Leu Cys Lys Gly Gly Gly Ala Val Pro Glu

             290 295 300

His   Ser Ala Asp His Asn Arg His Leu His Arg Pro Pro Cys Gly Arg
320   305 310 315

Ala   His Val Cys Gly Gly Leu Leu Gln Asn Gln Glu Thr Ala Glu Lys

             325 330 335

Asp   Ala Xaa Pro Ser Ser Ala Glu Pro Ser Val Xaa Thr Lys Gln Tyr

             340 345 350

Cys   Glu His Cys Gln Trp Ala Ser Pro Ser Xaa Pro Thr Pro Arg Glu

             355 360 365

Ala   Pro Ala Gly Glu Ser Ile Arg Ile Xaa Lys Arg His Leu Gln Xaa

             370 375 380

Tyr   Tyr Cys Xaa Glu Arg Ser Arg Asp Ile Leu Phe His Gln Ser Leu
400   385 390 395

Gln Phe His Ser Pro Ser Leu His Tyr Cys His Pro Asp Ser Xaa Pro
                 405   410   415

Cys Leu Glu Gln Arg Thr His Xaa Lys His Pro Phe Arg Lys Pro Leu
                 420   425   430

Trp Asn Arg Asp Val Ile Arg Arg Lys Gln Xaa Ala Gln Gln Pro Asn
                 435   440   445

Gly